RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: __10/001,453__

Source: __OIPE__

Date Processed by STIC: __12/11/01__

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE __CHECKER VERSION 3.0 PROGRAM__, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 10/001, 453

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
     Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
     prevent "wrapping."

2 _____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
     Numbering   use space characters, instead.

4 _____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
     ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
     each n or Xaa can only represent a single residue. Please present the maximum number of each
     residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
     "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
     previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
     the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
     Artificial or Unknown sequences.

7 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
     (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
     (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
     (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
     This sequence is intentionally skipped

     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
     (NEW RULES)   <210> sequence id number
     <400> sequence id number
     000

9 _____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
     (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
     In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
     Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
     is Artificial Sequence

11 _____ Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
     Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
     "Unknown." Please explain source of genetic material in <220> to <223> section.
     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
     "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
     listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

~~   CProject   ~~

 CProjectData   -Modified Acyl Carrier Proteins   09820.188
10/001453

Filed Herewith
2001-10-22   ~~

CDNASequence   seq1 Synthetic primerIccgcacatat gagcaccatc gaagaacgtg tg
32   agctrymkswbdhvn   DNA   ~~   CCommentFeature
        > I   ?   seq2 Synthetic primerIcaatactcga gttacgcctg
gtggccgttg atg
33   agctrymkswbdhvn   DNA   ~~   CIndivApplicant   Brian Fax

 G
?

Jeffrey Haas A

(sample of submitted file)

If PatentIn software was used to create the
above file, please contact Robert Wax at 703-306-4119
or 703-308-4216
for assistance

FYI   Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/001,453

DATE: 12/11/2001
TIME: 12:01:53

Input Set : A:\09820188.txt
Output Set: N:\CRF3\12112001\I001453.raw

Does Not Comply
Corrected Diskette Needed

```
       3 <110> APPLICANT: Fax, Brian G
       4        Haas, Jeffrey A
       6 <120> TITLE OF INVENTION: Modified Acyl Carrier Proteins
       8 <130> FILE REFERENCE: 09820.188
C-->  10 <140> CURRENT APPLICATION NUMBER: US/10/001,453
      11 <141> CURRENT FILING DATE: 2001-10-22
      13 <160> NUMBER OF SEQ ID NOS: 2
      15 <170> SOFTWARE: PatentIn version 3.1
      17 <210> SEQ ID NO: 1
      18 <211> LENGTH: 32
      19 <212> TYPE: DNA
      20 <213> ORGANISM: Synthetic primer
      22 <400> SEQUENCE: 1
      23 ccgcacatat gagcaccatc gaagaacgtg tg                              32
      26 <210> SEQ ID NO: 2
      27 <211> LENGTH: 33
      28 <212> TYPE: DNA
      29 <213> ORGANISM: Synthetic primer
      31 <400> SEQUENCE: 2
      32 caatactcga gttacgcctg gtggccgttg atg                             33
```

invalid response, see error summary sheet item 10

12/11/01

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/001,453

DATE: 12/11/2001
TIME: 12:01:54

Input Set : A:\09820188.txt
Output Set: N:\CRF3\12112001\I001453.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number